Figs. 1A and 1B. Schematic representation of the method of the present invention (DEXTAQ). A first polymerase of the present invention Fig. 1A which carries a "Tabor-Richardson" mutation for discriminating towards ddNTPs preferentially incorporates ddNTPs and produces the sequence ladder. A second polymerase of the present invention which, compared to the said first thermostable DNA polymerase Fig. 1B, has a reduced ability to incorporate dideoxynucleotides, preferably incorporates dNTPs and mainly produces products of full length and provides the uncoupled, direct, exponential amplification and sequence reaction with additional sequencing templates.

Please replace the paragraph beginning on page 13, the 5th line from the bottom (said paragraph ending on page 14, line 5) and the paragraph beginning on page 14, line 6 (said paragraph ending on page 14, line 10) with one combined paragraph as follows:

Figs. 2A-2F. 60 ng of total genomic DNA was subjected to a direct, uncoupled sequencing reaction using 6 pmol of an FITC-labelled primer (CCR5-2) and 3 pmol of an unlabelled primer (CCR5-1). The section shown in all figure panels is only at a distance of 20 base pairs from the end of the template and the last bases are part of the primer that generates the second template. No additional Taq DNA polymerase was added to the reaction that is shown in Fig. 2A. Increasing amounts of Taq DNA polymerase were added to the reactions that are shown in Fig. 2B (0.25 units), Fig. 2C (0.5 units), Fig. 2D (1.0 units) and Fig. 2E (2.0 units). In cases where no Taq DNA polymerase had been added, the A.L.F. software was not able to process a sequence. A better ratio between signal and noise is seen in the cases in which Taq DNA

polymerase had been added. In Fig. 2F, 60 ng of total genomic DNA was subjected to an uncoupled, direct amplification and sequencing reaction using equimolar amounts i.e. 3 pmol each of an FITC-labelled primer (CCR5-2) and of an unlabelled primer (CCR5-1). The A.L.F. software was able to process 290 bases. The reactions were carried out using 0.25 units Taq DNA polymerase and standard ThermoSequenase reagents.

D2 cont'd

Please replace the paragraph on page 14, lines 11-18 with the following:

Figs. 3A-3C. An uncoupled, direct, exponential amplification and sequencing reaction was carried out in combination with various thermostable polymerases which do not carry the "Tabor-Richardson" mutation. Fig. 3A shows a reaction in which 2.5 units Klentaq polymerase were added to a direct, uncoupled amplification and sequencing reaction which was carried out with 60 ng total genomic DNA. Fig. 3B shows a direct, uncoupled, exponential amplification and sequencing reaction which was carried out with standard Taq DNA polymerase and Fig. 3C shows a reaction in which 0.25 units Tth polymerase was added.

D3

IN THE CLAIMS

Kindly amend claims 41, 42 and 48 as set forth below.

41. (Amended) A process of claim 34, wherein the two primers are mobility modified and the amplified and chain terminated fragments are detected by electrophoresis.

D4